CLAIMS

1. An isolated polynucleotide which encodes a protein comprising the amino acid sequence of SEQ ID NO:3.

2. The isolated polynucleotide of Claim 1, wherein said protein has maltate dehydrogenase activity.

3. An isolated polynucleotide which comprises SEQ ID NO:2.

4. An isolated polynucleotide which is complimentary to the polynucleotide of Claim 3.

5. An isolated polynucleotide which is at least 70% identical to the polynucleotide of Claim 3.

6. An isolated polynucleotide which is at least 80% identical to the polynucleotide of Claim 3.

7. An isolated polynucleotide which is at least 90% identical to the polynucleotide of Claim 3.

8. An isolated polynucleotide which hybridizes under stringent conditions to the polynucleotide of Claim 3; wherein said stringent conditions comprise washing in 5X SSC at a temperature from 50 to 68°C.

9. The isolated polynucleotide of Claim 3, which encodes a protein having maltate dehydrogenase activity.

10. An isolated polynucleotide which comprises at least 15 consecutive nucleotides of the polynucleotide of Claim 3.

11. An isolated polypeptide which comprises the amino acid sequence of SEQ ID NO:3.

12. An isolated polypeptide which comprises the amino acid sequence of SEQ ID NO:1 and has maltate dehydrogenase activity.

13. A vector comprising the isolated polynucleotide of Claim 1.

14. A vector comprising the isolated polynucleotide of Claim 3.

15. A host cell comprising the isolated polynucleotide of Claim 1.

16. A host cell comprising the isolated polynucleotide of Claim 3.

17. The host cell of Claim 15, which is a *Coryneform* bacterium.

18. The host cell of Claim 16, which is a *Coryneform* bacterium.

19. The host cell of Claim 15, wherein said host cell is selected from the group consisting of *Coryneform glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium thermoaminogenes, Corynebacterium melassecola, Brevibacterium flavum, Brevibacterium lactofermentum,* and *Brevibacterium divaricatum.*

20. The host cell of Claim 16, wherein said host cell is selected from the group consisting of *Coryneform glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium thermoaminogenes, Corynebacterium melassecola, Brevibacterium flavum, Brevibacterium lactofermentum,* and *Brevibacterium divaricatum.*

21. A *Coryneform* bacterium which comprises an attentuated mdhA gene.

22. The *Coryneform* bacterium of Claim 21, wherein said mdhA gene comprises the polynucleotide sequence of SEQ ID NO:2.

23. *Eschericia coli* DSM 13494.

24. A process for producing L-amino acids comprising culturing the host cell of Claim 15 in a medium suitable for the expression of the polynucleotide; and collecting the L-amino acid.

25. The process of Claim 24, wherein said L-amino acid is L-lysine or L-glutamate.

26. The process of Claim 24, wherein said L-amino acid is L-lysine and the host cell further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of dapA, eno, zwf, pyc, and lysE.

27. The process of Claim 24, wherein said L-amino acid is L-lysine and the host cell further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, and poxB.

28. A process for producing L-amino acids comprising culturing the host cell of Claim 16 in a medium suitable for the expression of the polynucleotide; and collecting the L-amino acid.

29. The process of Claim 28, wherein said L-amino acid is L-lysine or L-glutamate.

30. The process of Claim 28, wherein wherein said L-amino acid is L-lysine and the host cell further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of wherein said gene is selected from the group consisting of dapA, eno, zwf, pyc, and lysE L.

31. The process of Claim 28, wherein the host cell further comprises at least one gene whose expression is

attenuated, wherein said gene is selected from the group consisting of pck gene, pgi gene, and poxB.

32. A process for producing L-amino acids comprising culturing the host cell of Claim 21 in a medium suitable for the expression of the polynucleotide; and collecting the L-amino acid.

33. The process of Claim 32, wherein said L-amino acid is L-lysine or L-glutamate.

34. The process of Claim 32, wherein said L-amino acid is L-lysine and the host cell further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of dapA, eno, zwf, pyc, and lysE.

35. The process of Claim 32, wherein said L-amino acid is L-lysine and the host cell further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, and poxB.

36. A process for screening for polynucleotides which encode a protein having the maltate dehydrogenase activity comprising hybridizing the isolated polynucleotide of Claim 1 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of maltate dehydrogenase activity in said protein.

37. A process for screening for polynucleotides which encode a protein having maltate dehydrogenase activity comprising hybridizing the isolated polynucleotide of Claim 3 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of maltate dehydrogenase activity in said protein.

38. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

39. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

40. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 3, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 3, or at least 15 consecutive nucleotides of the complement thereof.

41. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 3, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 3, or at least 15 consecutive nucleotides of the complement thereof.

42. A method for making maltate dehydrogenase, comprising: culturing the host cell of Claim 15 for a time and under conditions suitable for expression of the maltate dehydrogenase, and collecting the maltate dehydrogenase.

43. A method for making maltate dehydrogenase, comprising: culturing the host cell of Claim 16 for a time and under conditions suitable for expression of the maltate dehydrogenase B, and collecting the maltate dehydrogenase.